## METHODS, SOFTWARE AND APPARATI FOR IDENTIFYING GENOMIC REGIONS HARBORING A GENE ASSOCIATED WITH A DETECTABLE TRAIT

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Abstract of the Disclosure

The present invention relates to methods, software, and apparati for determining whether a genomic region harbors a gene associated with a detectable trait. In one embodiment, the present invention relates to a method of confirming that a genomic region harbors a gene associated with a detectable trait comprising the steps of identifying a candidate genomic region suspected of harboring the gene associated with the detectable trait, constructing a trait-associated distribution of association values using the biallelic markers in the candidate genomic region, identifying a plurality of biallelic markers in random genomic regions which are not suspected of harboring the gene associated with the detectable trait, constructing a random distribution of association values using the biallelic markers in the random genomic regions, comparing the trait-associated distribution of association values to the random distribution of association values, and determining whether the trait-associated distribution of association values are significantly different from one another. In other embodiments, the present invention comprises software for performing the above method and devices comprising the software in a retrievable form.

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